Rec'd PCT/PTO 30 JUN 1998

FORM PTO-1390 (REV 10-97) U S DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER	
760-248P	
U.S. APPLICATION NO. (If known, see 37 CFR 1.5)	
09/101132 NEW	

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/JP97/03946	October 30, 1997	October 30, 1996

TITLE OF INVENTION

c DNA FRAGMENT OF CAUSATIVE GENE OF SPINOCEREBELLAR ATAXIA TYPE2

APPLICANT(S) FOR DO/EO/US

TSUJI, Shoji; SANPEI, Kazuhiro

Applicant herewith submits to the Untied States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39 (1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☒ has been transmitted by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. 371(c)(3)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(2)).
   a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ have been transmitted by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been make and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.

12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.

13. ☒ A FIRST preliminary amendment.
    ☒ A SECOND or SUBSEQUENT preliminary amendment.

14. ☐ A substitute specification.

15. ☐ A change of power of attorney and/or address letter.

16. ☒ Other items or information:
    1). International Search Report
    2). Substitute Sequence Listing Paper & Disk Copy 14 Pages

U.S. APPLICATION NO (if known, see 37 CFR 1 5)	INTERNATIONAL APPLICATION NO	ATTORNEY'S DOCKET NUMBER
NEW	PCT/JP97/03946	760-248P

17. ☒ The following fees are submitted:

BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5):

Search Report has been prepared by the EPO or JPO **$930.00**

International preliminary examination fee paid to USPTO (37 CFR 1.482) **$720.00**

No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)). . . . **$790.00**

Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO **$1,070.00**

International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4). **$98.00**

CALCULATIONS PTO USE ONLY		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$ 930.00	
Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(e)).	$ 0.00	

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total Claims	13 - 20 =	0	X **$22.00**	$ 0.00	
Independent Claims	1 - 3 =	0	X **$82.00**	$ 0.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)		YES	+ **$270.00**	$ 270.00	
			TOTAL OF ABOVE CALCULATIONS =	$ 1,200.00	
Reduction of ½ for filing by small entity, if applicable. Verified Small Entity statement must also be filed (Note 37 CFR 1.9, 1.27, 1.28).				$ 0.00	
			SUBTOTAL =	$ 1,200.00	
Processing fee of **$130.00** for furnishing the English translation later than ☐20 ☐30 months from the earliest claimed priority date (37 CFR 1.492(f)). +				$ 0.00	
			TOTAL NATIONAL FEE =	$ 1,200.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). **$40.00** per property +				$ 40.00	
			TOTAL FEES ENCLOSED =	$ 1,240.00	
			Amount to be: refunded	$	
			charged	$	

a. ☒ A check in the amount of $ **1,240.00** to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account. No. _____ in the amount of $_____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-2448. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

Send all correspondence to:
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32350
SIGNATURE

MURPHY, GERALD M., JR.
NAME

28,977
REGISTRATION NUMBER

/aam June 30, 1998

IN THE U. S. PATENT AND TRADE MARK OFFICE

APPLICANT: Shoji TSUJI et al.

INT'L. APPLN. NO.: PCT/JP97/03946

SERIAL NO.: New GROUP:

FILED: June 30, 1998 EXAMINER:

FOR: cDNA FRAGMENT OF CAUSATIVE GENE OF SPINOCEREBELLAR ATAXIA TYPE2

PRELIMINARY AMENDMENT

Honorable Commissioner of Patents
BOX PATENT APPLICATION
Washington, D.C. 20231

June 30, 1998

Sir:

The following Preliminary Amendment and Remarks are respectfully submitted in connection with the above-identified application.

IN THE SPECIFICATION:

Before line 1, insert --This application claims the benefit under 35 U.S.C. §371 of prior PCT International Application No. PCT/JP97/03946 which has an International filing date of October 30, 1997 which designated the United States of America, the entire contents of which are hereby incorporated by reference.--

R E M A R K S

The specification has been amended to provide a cross-reference to the previously filed International Application.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account 02-2448 for any additional fees required under 37 C.F.R §1.16 or under 37 C.F.R. §1,17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH, BIRCH, LLP

By _____

Gerald M. MURPHY
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PATENT
760-248P

IN THE U.S. PATENT AND TRADEMARK OFFICE

Applicant(s):	Shoji TSUJI, Kazuhiro SANPEI		
Application No.:	NEW	Group No.:	
Filed:	June 30, 1998	Examiner:	
For:	cDNA FRAGMENT OF CAUSATIVE GENE OF SPINOCEREBELLAR ATAXIA TYPE 2		

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

June 30, 1998

Dear Sir:

Preliminary to the examination of the above-referenced NEW U.S. patent application, the following amendments and remarks are respectfully submitted.

IN THE SPECIFICATION:

Page 3

Line 5, change "SEQ ID NO: 1" to --SEQ ID NO:2--

Page 4

Line 11, after "sequence " insert --(SEQ ID NO:1)--

Page 5

Line 6, change "ID NO: 1" to --ID NO:2--

Line 13, change "SEQ ID NO: 1" to --SEQ ID NO:2--

Page 12

Line 3, after "$(CAG)_{56}$" insert --(SEQ ID NO:6)--

Line 5, after "CC-3' " insert --(SEQ ID NO:3)--

Line 7, after first occurrence of "3' " insert --(SEQ ID NO:4)--

Line 7, after "TG-3' " insert --(SEQ ID NO:5)--

Page 15

Line 9, after "AGC-3' " insert --(SEQ ID NO:7)--

Line 10, after "3' " insert --(SEQ ID NO:8)--

Page 16

Line 11, after "C-3' " insert --(SEQ ID NO:9)--

Line 20, after "ACC-3' " insert --(SEQ ID NO:10)--

Page 17

Line 3, after "C-3' " insert --(SEQ ID NO:11)--

Line 4, after "CG-3' " insert --(SEQ ID NO:12)--

Page 18

Line 9, after "C-3' " insert --(SEQ ID NO:13)--

Please replace pages 21-33 with the Substitute Sequence Listing enclosed herewith. Please renumber the remaining pages of the Specification, beginning with the Claims consecutively from page 35 of the Substitute Sequence Listing.

IN THE CLAIMS:

Claim 1, line 2: after "sequence " insert --as--.

Remarks

Enclosed herewith in full compliance with 37 C.F.R. 1.821-1.825 is a Substitute Sequence Listing to be inserted into the specification as indicated above. The Substitute Sequence Listing in no way introduces new matter into the specification.

Also submitted herewith in full compliance with 37 C.F.R. 1.821-1.825 is a disk copy of the Substitute Sequence Listing. The disk copy of the Substitute Sequence Listing, file 760-248.SUB, is identical to the paper copy, except that it lacks formatting.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees requires under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

Respectfully submitted,

BIRCH, STEWART, KOLASCH & BIRCH, LLP

By _____
Gerald M. Murphy, Jr.
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760-248P

Enclosures: Paper and Disk copy of Substitute Sequence Listing

DESCRIPTION

cDNA Fragment of Causative Gene of Spinocerebellar Ataxia Type 2

TECHNICAL FIELD

The present invention relates to cDNA fragments of the causative gene of spinocerebellar ataxia type 2 (hereinafter also referred to as "SCA2"), proteins encoded thereby, antibodies corresponding to the proteins, and antisense nucleic acids of the above-mentioned cDNA fragments.

BACKGROUND ART

SCA2 is an autosomal dominant, neurodegenerative disorder that affects the cerebellum and other areas of the central nervous system.

It has recently been discovered that the causative genes of 6 neurodegenerative diseases including dentatorubral-pallidoluysian atrophy (DRPLA) have more CAG repeats than the normal genes. That is, the numbers of CAG repeats in the causative genes of the neurodegenerative diseases are 37 to 100, while those in the normal genes are less than 35.

It has been suggested that the causative gene of SCA2 has an increased number of CAG repeats (Trottier, Y. et al. *Nature*, 378, 403-406 (1995)). However, since the causative gene of SCA2 has not been identified, and since its nucleotide sequence has not been determined, SCA2 cannot be diagnosed by a genetic assay.

DISCLOSURE OF THE INVENTION

An object of the present invention is to provide a sequence-determined cDNA fragment of the causative gene of SCA2. Another object of the present invention is to provide a protein produced by the causative gene of SCA2. Still another object of the present invention is to provide an antibody specific to the above-mentioned protein, which antibody is useful for therapy and diagnosis of SCA2. Still another object of the present invention is to provide an antisense of the causative gene of SCA2, which is useful for therapy of SCA2.

The present inventors intensively studied to discover a *Tsp* E1 fragment with a size of 2.5 kb in which the number of CAG triplet is increased only in SCA2 patients, and partial sequence thereof was determined. Human cDNA library was screened using as probes the oligonucleotides that respectively hybridize with the regions between which the CAG triplet repeats are interposed, and a cDNA fragment which hybridizes with both of these two probes was cloned. Using this cDNA fragment as a probe, human cDNA library was screened and a plurality of cDNA fragments which hybridize with the probe were cloned. Sequencing the cDNA fragments revealed that these cDNA fragments overlap with each other. To sequence the 5'-end and 3'-end regions, RACE (rapid amplification of cDNA ends) was performed. Further, to sequence the 5'-end region, RT-PCR was

performed, thereby succeeding in sequencing the full length of the cDNA of the causative gene of SCA2.

That is, the present invention provides a nucleic acid fragment comprising a nucleic acid region encoding an amino acid sequence shown in SEQ ID NO: 1 (provided that the number of repeat units of Gln from the 166th to 188th amino acid varies between 15 and 100). The present invention also provides a protein having an amino acid sequence encoded by the nucleic acid fragment according to the present invention. The present invention further provides an antibody which undergoes antigen-antibody reaction with the above-mentioned protein. The present invention still further provides an antisense nucleic acid having a size of not less than 15 bp, which hybridizes with a mRNA transcribed from the nucleic acid fragment according to the present invention so as to inhibit translation thereof.

By the present invention, a sequence-determined cDNA fragment of the causative gene of SCA2 was provided. The protein encoded by the nucleic acid fragment according to the present invention may be used for therapy of SCA2 and may be used as an immunogen for preparing an antibody useful for therapy and diagnosis of SCA2. Further, since the nucleotide sequence of the causative gene of SCA2 was determined by the present invention, antisense to this gene may now be designed. Still further, by the present invention, a recombinant vector comprising the nucleic

acid fragment according to the present invention which is incorporated in an expression vector that can express a desired gene in human body, which recombinant vector can express the nucleic acid fragment in human body, as well as a method for expressing the nucleic acid fragment according to the present invention comprising introducing the recombinant vector into human body. Thus, the present invention is thought to largely contribute to the therapy and diagnosis of SCA2.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 shows the nucleotide sequence of the cDNA fragment according to the present invention together with the amino acid sequence encoded thereby, which nucleotide sequence was determined in the Examples of the present invention.

Fig. 2 shows the continuation of Fig. 1.

Fig. 3 shows the continuation of Fig. 2.

Fig. 4 shows the continuation of Fig. 3.

Fig. 5 is a pedigree chart of the SCA2 patients who donated the genomic DNAs used in the Examples.

Fig. 6 shows the sizes, positions and restriction sites of the genomic DNA fragments Tsp1 and Tsp2, and SCA2 cDNA obtained in the Examples of the present invention, as well as the size and position of each of the obtained cDNA fragment.

Fig. 7 shows the distribution of the numbers of the CAG repeat units in the normal and SCA2 genes, which were

measured by using the $(CAG)_{55}$ probe.

BEST MODE FOR CARRYING OUT THE INVENTION

As described above, the nucleic acid fragment according to the present invention comprises the nucleic acid region encoding the amino acid sequence shown in SEQ ID NO: 1 in the SEQUENCE LISTING, provided that the number of repeating units of Gln from the 166th to the 188th amino acid varies between 15 and 100. The number of this repeat units is 15 to 25 in normal individuals and 35 to 100 in SCA2 patients. As is well-known, due to degeneration, there are a plurality of codons encoding one amino acid, and any nucleic acids which encode the amino acid sequence shown in SEQ ID NO: 1 are included within the scope of the present invention. The nucleotide sequence actually determined in the Examples below is shown in SEQ ID NO:1 and in Figs. 1-4. The way how the nucleotide sequence was determined and the fact that the cDNA having this nucleotide sequence is the cDNA of the causative gene of SCA2 are detailed in the Examples below.

The nucleic acid fragment according to the present invention may be cloned by the method detailed in the Examples below. Further, since the nucleotide sequence of the nucleic acid fragment according to the present invention was determined by the present invention, the nucleic acid fragment may be cloned by utilizing amplification by PCR using human cDNA library as a

template, or by hybridization using the PCR product as a probe. In cases where it is difficult to amplify the nucleic acid fragment by a single PCR, the nucleic acid fragment may be divided into a plurality of regions and the PCR products may be ligated by a conventional method so as to clone the nucleic acid fragment.

By incorporating the nucleic acid fragment according to the present invention into the multicloning site of a commercially available expression vector, and by transforming host cells with the obtained recombinant vector, the protein encoded by the nucleic acid fragment may be produced. Host-vector systems for expressing an arbitrary gene in a host cell is well-known in the art and a number of host-vector systems are commercially available. Those skilled in the art may easily express the nucleic acid fragment according to the present invention so as to produce the protein using such a commercially available host-vector system. Such a well-known method is described in, for example, D. M. Glover, DNA Cloning Volume III a practical approach, 1987, IRL Press.

For example, according to a conventional method, the nucleic acid fragment according to the present invention may be amplified by the long PCR (LA PCR) (Hiroyuki MUKAI, PROTEIN, NUCLEIC ACID, ENZYME, Vol.41, No.5, 585-594, 1996) using primers in which restriction sites are introduced, and the amplified product is digested with a

restriction enzyme. The digested amplified product is then inserted into the multicloning site of a commercially available plasmid vector pGEX (PHARMACIA) and ligated to obtain a recombinant vector, followed by transforming *E. coli* DH5α (GIBCO BRL) by the conventional calcium chloride method. Transformants are then selected based on the drug resistance (ampicillin resistance) and the protein encoded by the causative gene of SCA2 may be recovered from the transformants. In cases where this vector is used, the desired protein is obtained as a fusion protein with GST (Glutathion S-Transferase), so that the protein may easily be detected using a commercially available anti-GST antibody (PHARMACIA).

Since the active protein produced by the gene of normal individuals (the number of CAG repeats is 15 to 25) is thought to have the normal function, SCA2 may be treated or alleviated by administering the normal protein to SCA2 patients. However, since SCA2 is autosomal dominant, it is necessary to simultaneously block the causative gene of SCA2 of the patient with the antisense described below.

By immunizing an animal with the above-described protein or an antigenic fragment thereof, an antibody specific to the protein or the fragment thereof may be recovered from the animal by a conventional method. The antibody may be a polyclonal antibody or a monoclonal antibody, and the monoclonal antibody may be prepared by

a well-known method.

It is theoretically difficult to construct an antibody using the polyglutamine chain encoded by the CAG repeat, which antibody has varying reactivities with the polyglutamine chain depending only on the lengths of the polyglutamine chain. However, by using the full length protein which was clarified by the present invention, an antibody which recognizes the stereoscopic difference between the patient's protein and the normal protein may be prepared. Further, by virtue of the present invention, since an antibody may be prepared by using a region of the SCA2 product, which is common to the normal individuals and the patients, a control is available in any assay system using an antibody specific to the protein according to the present invention. Using such an antibody, a simple assay such as plate method may be attained by a conventional method.

An affinity column may be prepared by immobilizing the antibody according to the present invention on agarose gel (e.g., Sephadex (trademark) of PHARMACIA), polystyrene beads or the like and by packing the resultant in a column. By passing a body fluid (blood, serum, spinal fluid or the like) through the affinity column, the protein produced by the causative gene of SCA2 of the patient may be obtained. By eluting the protein and by measuring the molecular weight thereof, diagnosis of SCA2 may be attained. This is because that

the protein of a SCA2 patient has a molecular weight larger than that of the protein of a normal individual because the number of CAG repeat units of the SCA2 causative gene in the patient is larger than that of the gene in the normal individual.

Possible gene therapies include the method by which production of the abnormal SCA2 gene product is stopped and the method by which normal SCA2 gene product is introduced. The former method includes blocking of translation of mRNA using an antisense. The latter method includes administration of the SCA2 gene product prepared *in vitro*, and introduction of the nucleic acid fragment into the cells. Since in patients suffering from SCA2 caused by extension of the CAG repeat, the abnormal protein is dominant, it is thought that the desired effect may be obtained by simultaneously performing both of the above-mentioned methods. In this case, the antisense is designed such that it hybridizes with a region not affecting the activity of the SCA2 product, and the region is removed from the normal SCA2 gene to be introduced, thereby assuring that the antisense does not inhibit the production of the normal protein. By designing the antisense and the normal SCA2 gene as mentioned above, the antisense and the SCA2 gene may be incorporated in the same vector and the vector may be introduced into cells.

The antisense nucleic acid according to the present

invention hybridizes with the mRNA transcribed from the nucleic acid fragment according to the present invention, and has a size of preferably not less than 15 bp and not more than the full length of the coding region of the nucleic acid fragment, more preferably not less than 50 bp and not more than the full length of the coding region of the nucleic acid fragment. Although the antisense nucleic acid preferably has a nucleotide sequence completely complementary to the entire mRNA or a part thereof, transcribed from the nucleic acid fragment according to the present invention, those having homologies to the degree that they hybridize with the mRNA *in vivo* are within the scope of the present invention. By administering the antisense according to the present invention to an SCA2 patient, the causative gene of SCA2 may be blocked. By administering the above-mentioned protein from a healthy individual to the patient under this condition, SCA2 may be treated or alleviated. The dose of the antisense nucleic acid may be appropriately selected depending on the conditions of the patient, and may usually be 0.001 mmol to 1000 mmol per day per 1 kg of bodyweight.

Known methods for introducing the gene into the body include methods in which Retrovirus or Adenovirus is used as a vector (Yasuhiro SETOGUCHI, Experimental Medicine, Vol.12, No.15 (extra edition) 1994, pp.114-121; Hiromi KANEGAE et al., Experimental Medicine, Vol.12, No.15

(extra edition) 1994, pp.34-40), methods using liposomes, and methods using fusion liposomes (membrane-fused liposome and the like). Among these, since Adenovirus expresses the introduced gene without proliferation of the target cells, the method utilizing Adenovirus is most appropriate as the method for introducing the nucleic acid into nervous system. More particularly, E3 and a part of E1a of the DNA of wild type Adenovirus type 5 are removed and the nucleic acid in double-stranded form is introduced into the virus together with an expression unit such as a promoter. The recombinant virus vector is proliferated in 293 cells expressing E1a and E1b genes, originated from human fetal kidney to prepare a virus liquid, and the virus liquid is inoculated. The virus genome incorporated into the nucleus of the cell exists outside the chromosomes without replication. Since the virus genome is not lost by cell division in nerve cells, expression of normal SCA2 gene may be maintained for 1 to 3 months.

The present invention will now be described more concretely by way of examples thereof. It should be noted that the present invention is not restricted to the following examples.

Example 1 Preparation of $(CAG)_{55}$ Probe

A genomic DNA segment of DRPLA gene containing a CAG repeat with 55 repeat units was amplified from the genomic DNA of a patient with DRPLA (Koide, R. et al.,

Nature Genet., 6, 9-13 (1994)) and was subcloned into a plasmid vector, pT7Blue T(*p-2093*). The *p-2093* plasmid contains the $(CAG)_{55}$ and the flanking sequences. That is, the plasmid contains the sequence of 5'-CAC CAC CAG CAA CAG CAA $(CAG)_{55}$ CAT CAC GGA AAC TCT GGG CC-3'. Using a pair of oligonucleotides 5'-CAC CAC CAG CAA CAG CAA CA-3'and 5'-biotin-GGC CCA GAG TTT CCG TGA TG-3', PCR was performed in a total volume of 16 µl containing 10 mM Tris-HCl, pH8.3, 50 mM KCl, 1.5 mM $MgCl_2$, 2M N,N,N-trimethylglycine, 0.1 mM TTP, 0.1 Mm dCTP, 0.1 mM dGTP, 9.25 MBq of [α-^{32}P]dATP (222 TBq/mmol), 0.5 µM each of the two primers, 0.3 ng of plasmid DNA (*p-2093*) and 2.0 U of Taq DNA polymerase (Takara Shuzo, Kyoto, Japan). After an initial 2-min. denaturation at 94°C, PCR was performed for 30 cycles consisting of 1-min. denaturation at 94°C, 1-min. annealing at 54°C and 3-min. extension at 72°C, followed by a final extension at 72°C for 10 min.

A single-stranded $(CAG)_{55}$ probe was isolated using streptavidin-coated magnetic beads (Dynabeads M-280, Streptavidin;Dynal AS, Oslo, Norway) on which 20 µl of streptavidin is coated. That is, after washing of the PCR products immobilized on the magnetic beads with 40 µl of a solution containing 5 mM Tris-HCl (pH 7.5), 0.5 mM EDTA and 1 M NaCl, the non-biotinylated strand containing the radio-label was separated from the biotinylated strand by incubation in 50 µl of 0.1 M NaOH for 10 min. The resultant supernatant was directly added to the

hybridization solution described below.

Incidentally, using the single-stranded $(CAG)_{55}$ probe prepared as described above, Southern blot analysis was carried out on the androgen receptor genes containing 9, 22, 43 and 51 CAG repeat units, respectively. As a result, the $(CAG)_{55}$ probe strongly hybridized with the genes having 43 and 51 CAG repeats units, respectively, but scarcely hybridized with the gene having 22 CAG repeat units, and did not hybridize at all with the gene having 9 CAG repeat units (K. Sanpei et al., Biochemical and Biophysical Research Communications, Vol.212, No.2, 1995, pp.341-346). Thus, by using this probe, hybridization may be selectively attained only with DNAs containing a number of (e.g., 35 or more) CAG repeat units if the hybridization conditions are appropriately selected.

(2) Determination of Nucleotide Sequence of SCA2 Gene

Fig. 5 shows a pedigree chart of SCA2 patients. In this pedigree chart, males are represented by squares and females are represented by circles. SCA2 patients are represented by black squares or circles, and unaffected persons are represented by white squares or circles.

High-molecular-weight genomic DNA (15 μg) was digested with 100 U of *TspE*I (Toyobo, Osaka, Japan), electrophoresed through 0.8% agarose gels and transferred to nitrocellulose membranes. The membranes were hybridized with the $(CAG)_{55}$ probe described above.

Hybridization was performed in a solution containing 2.75 x SSPE (1 x SSPE=150 mM NaCl, 10 mM NaH_2PO_4, 1 mM EDTA), 50% formamide, 5 x Denhardt's solution, 100 ng/ml of sheared salmon sperm DNA and the $(CAG)_{55}$ probe (6×10^6 cpm/ml) at 62°C for 18 hours. After the hybridization, the membranes were washed with 1 x SSC (150 mM NaCl, 15 mM sodium citrate) containing 0.5% SDS at 65°C for 0.5 hours. The membranes were autoradiographed for 16 hours to Kodak Bio Max MS film at -70°C using an MS intensifying screen.

As a result, 2.5 kbp *TspE*I fragment hybridized with the probe was detected only in all of the SCA2 patients.

Genomic DNA (270 µg) from an SCA2 patient (individual 7 in Fig. 5) was digested by *TspE*I and subjected to agarose gel electrophoresis. Genomic DNA fragments including the 2.5 kb *TspE*I fragment were cloned into an *Eco*RI-cleaved λZAPII vector. The genomic library was screened using the $(CAG)_{55}$ probe under the hybridization condition described above. A genomic clone, *Tsp*-1, containing an expanded CAG repeat was isolated.

After removal of the probe, the above-described genomic library was screened again using the *Tsp-1* as a probe, which was labeled by the random priming. Hybridization was carried out in a solution containing 5 x SSC, 1 x Denhardt's solution, 10% dextran sulfate, 20 mM sodium phosphate, 400 µg/ml human placental DNA and the *Tsp-1* probe at 42°C for 18 hours. After the

hybridization, the membranes were washed finally in 0.1 x SSC - 0.1% SDS at 52°C for 0.5 hours. The membranes were autoradiographed for 24 hours to Kodak Bio Max MS films at -70°C using an MS intensifying screen. As a result, a genomic clone, *Tsp-2*, originated from a normal allele was isolated.

The SmaI-ApaI fragment (630 bp) of Tsp2 was sequenced and oligonucleotides F-1 (5'-CCC TCA CCA TGT CGC TGA AGC-3') and R-1 (5'-CGA CGC TAG AAG GCC GCT G-3') were designed such that the CAG repeat units are sandwiched between the oligonucleotides (see Fig. 1). Using oligonucleotides F-1 and R-1 as probes, human procephalic cortex cDNA library (STRATAGENE) was screened. Hybridization was performed in a solution containing 6 x SSC, 10 x Denhardt's solution, 0.5% SDS, 0.05% sodium pyrophosphate, 100 ng/ml of sheared salmon sperm DNA and end-labeled oligonucleotide probes at 55°C for 18 hours. After the hybridization, the membrane was finally washed with 6 x SSC containing 0.5% SDS and 0.05% sodium pyrophosphate at 55°C for 0.5 hours. A cDNA clone Fc1 with a size of 4.0 kb which hybridized with the both probes was obtained. The nucleotide sequences of Fc1, Tsp1 and Tsp2 were determined and compared. As a result, the nucleotide sequences in the vicinities of the CAG repeat units were identical except for the number of the CAG repeat units. Restriction maps of Tsp1 and Tsp2, as well as the sizes and positions of Fc1 and other

fragments hereinbelow described, are shown in Fig. 6. Using Fc1 or a fragment isolated by the screening later described as a probe, human cDNA libraries (human procephalic cortex, human fetal brain, human brain and brain stem) were screened to isolate cDNA clones Fc2, Fb14, B4, C6 and C19 (see Fig. 6). To identify the 5'-end of Fc1, 5'-RACE (Frohman, M.A. et al, Proc. Natl. Acad. Sci. USA 85, 8998-9002 (1988)) was performed using 5'-RACE-Ready cDNA (Clonetech, Palo Alto, CA, USA). Primer R-1 was used for the first PCR, and Primer R-2 (5'-CTT GCG GAC ATT GGC AGC C-3', see Fig. 1) was used for the second PCR. In both PCRs, F-1 (see Fig. 1) was used as the forward primer. The 5'-RACE product (5R1) having the size of 350 bp was subcloned into pT7Blue T vector (pT7Blue T-vector (5R1)). The identification of 5R1 was confirmed by the overlapping with the nucleotide sequences of Fc1, Tsp1 and Tsp2. To identify the 3'-end of the cDNA, 3'-RACE was performed using 1 μg of poly(A)$^+$mRNA extracted from human brain as a template and Primer F-13 (5'-TTC TCT CAG CCA AAG CCT TCT ACT ACC-3', see Fig. 3) as a primer. The obtained 3'-RACE product (3R1) with a size of 1300 bp was subcloned into pT7Blue T vector (pT7Blue T-vector (3R1)).

To investigate the 5'-end region of the cDNA, reverse transcription PCR (RT-PCR) was performed. That is, total RNAs extracted from an autopsy from human brain were digested by RNase-free DNase (PROMEGA) (Onodera, O.

et al., Am. J. Hum. Geent. 57, 1050-1060(1995)). As the primers for the PCR, F1006 (5'-TAT CCG CAG CTC CGC TCC C-3', see Fig. 1) and R1002 (5'-AGC CGG GCC GAA ACG CGC CG-3') were used. PCR was performed in a solution with a total volume of 20 μM, which contained 5 pmol each of the each primer, 10 mM Tris HCl (pH8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 1.7M N,N,N-trimethylglycine, 200 μM each of dATP, dCTP and TTP, 100 μM of dGTP, 100 μM of 7-deaza dGTP and 2.5 U of Taq polymerase (TAKARA SHUZO). After carrying out the initial denaturation at 96°C for 2 minutes, a cycle of a denaturation step at 96°C for 1 minute, an annealing step at 65°C for 1 minute and an extension step at 72°C for 1 minute were repeated 30 times, and a final extension step at 72°C for 5 minutes was performed, thereby carrying out the PCR. As a result, a clone 5R1 which extends upstream of 5R1 by 246 bp was obtained (see Fig. 6).

In Fig. 6, the hollow regions in the Tsp1 and Tsp2 fragments indicate the regions which exist in SCA2 cDNAs. The hollow regions in the SCA2 cDNA shows coding regions. The CAG repeating regions are shown as solid boxes. Restriction sites TspE1 (T)、NotI (N)、Sac II (S)、Sau3AI (Sa)、Sma I (Sm)、Eco52I (E52)、Apa I (Ap)、AccI (Ac)、BamHI (B)、XhoI (X)、EcoRI (E) and Pst I (P) are shown. The size and position of each cDNA clone are shown below the consensus SCA2 cDNA.

In this example, nucleotide sequences of double-

stranded DNAs were determined by the dideoxynucleotide chain termination method (Sanger, F. et al. Proc. Natl. Acad. Sci. USA 74, 5463-5467(1977); Chen E.Y. et al, DNA 4, 165-170 (1985)) using a double-stranded plasmid DNA as a template. To determine the nucleotide sequences of the CAG repeating regions and their flanking regions, genomic fragments containing the CAG repeating regions were amplified by PCR using biotinylated F-1 and RS-1 (5'-CCT CGG TGT CGC GGC GAC TTC C-3'). PCR was performed in a solution with a total volume of 25 µl, which contained 0.25 µM each of the each primer, 10 mM Tris HCl (pH8.3), 50 mM KCl, 2.0 mM $MgCl_2$, 1.7M N,N,N-trimethylglycine, 200 µM each of dNTP, 200 ng of the genomic DNA and 1.25 U of Taq polymerase (TAKARA SHUZO). After carrying out initial denaturation at 95°C for 1 minute, a cycle of a denaturation step at 95°C for 2 minutes, an annealing step at 62°C for 1 minute and an extension step at 72°C for 1 minute was repeated 32 times, and a final extension step at 72°C for 5 minutes was performed, thereby carrying out the PCR. Biotinylated chains were recovered using streptavidin-coated magnetic beads and were directly sequenced.

Based on the nucleotide sequences of the above-mentioned cDNA clones, a consensus SCA2 cDNA sequence with a length of 4351 bp excluding the poly A tail was determined (SEQ ID NO:1, Figs. 1-4, see Fig. 6). In SEQ ID NO: 1, the region from 4352nt to 4367nt is the poly A

tail, and the number of "A" is not restricted to that shown in SEQ ID NO: 1. It was confirmed that the poly A tail exists at the same location in C19, B4 and 3R1 which were independent cDNA clones.

Example 2 Measurement of CAG Repeat Units in Sample

Numbers of CAG repeat units were determined by polyacrylamide gel electrophoresis analysis of PCR products obtained using the primer pair of F-1 and R-1. PCR was performed in a total volume of 10 µl containing 10 mM Tris-HCl, pH 8.3, 50 mM KCl, 2.0 mM $MgCl_2$, 1.7 M *N,N,N*-trimethylglycine, 111KBq of [α-^{32}P]dCTP (111 Tbq/mmol), 30 µM dCTP, and 200 µM each of dATP, dGTP and TTP, 0.25 µM each of the two primers, 200 ng of genomic DNA and 1.25 U of Taq DNA polymerase. After an initial 2-min denaturation at 95°C, PCR was performed for 32 cycles of 1-min denaturation at 95°C, 1-min annealing at 60°C and 1-min extension at 72°C, followed by a final extension at 72°C for 5 min. Sequence ladders obtained using the cloned genomic segments of the SCA2 gene, which contain various sizes of CAG repeats, were used as size markers. For normal alleles containing one or two CAA interruptions, the numbers of the CAA units were included in the CAG repeat size. For SCA2 alleles having expanded CAG region, the above-mentioned insert sequence immediately after the CAG region was not included in the size of the CAG region.

By the above-described method, the numbers of the

CAG repeat units of normal individuals (286 chromosomes) and 10 pedigrees of SCA2 patients (34 SCA2 chromosomes) were determined. The results are shown in Fig. 7. In Fig. 7, open bars indicate the results of the normal genes and solid bars indicate the results of the SCA2 genes.

As is apparent from Fig. 7, in all of the normal genes, the numbers of the CAG repeat units were not more than 24, while in all of the SCA2 genes, they were not less than 35. Thus, it was confirmed that the cDNA identified as described above is the cDNA of the causative gene of SCA2.

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 4367

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION

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TATCCGCACC TCCGCTCCCA CCCGGCGCCT CGGCGCGCCC GCCCTCCG ATG CGC TCA    57
                                                      Met Arg Ser
                                                      1

GCG GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC    105
Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg
    5                  10                  15

TTC GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG    153
Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala
20                  25                  30                  35

CGG CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC    201
Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro
                40                  45                  50

TCC GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG    249
Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln
            55                  60                  65

AGC TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC    297
Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly
        70                  75                  80

GGC GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG    345
Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Gly
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    85                  90                  95
CCT CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC    393
Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly
100                 105                 110                 115
GCC CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG    441
Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala
                120                 125                 130
TCC CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT    489
Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys
            135                 140                 145
CCC CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG    537
Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu
        150                 155                 160
AAG CCC CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAA    585
Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
    165                 170                 175
CAG CAG CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT    633
Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn
180                 185                 190                 195
GTC CGC AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG    681
Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala
                200                 205                 210
CCT TCG CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC    729
Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro
            215                 220                 225
TCC TCG GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC    777
Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly
        230                 235                 240
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AGA GGT CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT 825
Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe
245 250 255
GAT GGA ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT 873
Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val
260 265 270 275
GTT GGC TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA 921
Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu
280 285 290
GGA GTT TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC 969
Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala
295 300 305
GCA CAT GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA 1017
Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu
310 315 320
ATA ATG GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG 1065
Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln
325 330 335
TTT AAA GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC 1113
Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp
340 345 350 355
TCT GCT ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG 1161
Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu
360 365 370
GAG CCC TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT 1209
Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala
375 380 385
TTG GAA AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA 1257

Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg

390 395 400

TAT AAT GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA 1305

Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu

405 410 415

TCT TCG TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA 1353

Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu

420 425 430 435

AAA CGG GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT 1401

Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser

440 445 450

GCC CAG TAC AAA GCT CGA GTG GCC CTG GAA AAC GAT GAT AGG AGT GAG 1449

Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu

455 460 465

GAA GAA AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG 1497

Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly

470 475 480

CAC AGC ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA 1545

His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg

485 490 495

AAT AGA GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT 1593

Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg

500 505 510 515

ATG GGC CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC 1641

Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His

520 525 530

ACT TCA GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT 1689

Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn

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                535                 540                 545
GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA   1737
Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro
        550                 555                 560
CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC   1785
Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala
    565                 570                 575
ACC CCT ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC   1833
Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro
580                 585                 590                 595
CCG TCT CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG   1881
Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met
                600                 605                 610
CCT AAA CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC   1929
Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala
            615                 620                 625
CAG CGA CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA   1977
Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile
        630                 635                 640
TCC AGT GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT   2025
Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala
    645                 650                 655
ACT CCT CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA   2073
Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser
660                 665                 670                 675
GTG GTC AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG   2121
Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg
                680                 685                 690
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TCT CCC AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT 2169
Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu
695 700 705

GCT TCT CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT 2217
Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro
710 715 720

ATT CCA GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT 2265
Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala
725 730 735

GTT ACC CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG 2313
Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg
740 745 750 755

CAG AAC TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA 2361
Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr
760 765 770

TCA CCT AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT 2409
Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val
775 780 785

TCT GAA CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT 2457
Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp
790 795 800

TTT AGG TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA 2505
Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu
805 810 815

AAC AAA AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA 2553
Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys
820 825 830 835

ATT GAA CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC 2601

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Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn
                840                 845                 850
TGT ACC AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA   2649
Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser
            855                 860                 865
ATA CTT AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA   2697
Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln
        870                 875                 880
GGG GTT CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG   2745
Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys
    885                 890                 895
GAA GAG AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT   2793
Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn
900                 905                 910                 915
CCC AAT GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT   2841
Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro
                920                 925                 930
TCT ACT ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT   2889
Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser
            935                 940                 945
ATG GTG GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT   2937
Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys
        950                 955                 960
TTT GCA CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA   2985
Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro Gly Val Gln
    965                 970                 975
CCT TTA TAC CCA ATA CCT ATG ACG CCC ATG CCA GTG AAT CAA GCC AAG   3033
Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn Gln Ala Lys
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980 985 990 995

ACA TAT AGA GCA GTA CCA AAT ATG CCC CAA CAG CGG CAA GAC CAG CAT 3081

Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln Asp Gln His

1000 1005 1010

CAT CAG AGT GCC ATG ATG CAC CCA GCG TCA GCA GCG GGC CCA CCG ATT 3129

His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly Pro Pro Ile

1015 1020 1025

GCA GCC ACC CCA CCA GCT TAC TCC ACG CAA TAT GTT GCC TAC AGT CCT 3177

Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala Tyr Ser Pro

1030 1035 1040

CAG CAG TTC CCA AAT CAG CCC CTT GTT CAG CAT GTG CCA CAT TAT CAG 3225

Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro His Tyr Gln

1045 1050 1055

TCT CAG CAT CCT CAT GTC TAT AGT CCT GTA ATA CAG GGT AAT GCT AGA 3273

Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly Asn Ala Arg

1060 1065 1070 1075

ATG ATG GCA CCA CCA ACA CAC GCC CAG CCT GGT TTA GTA TCT TCT TCA 3321

Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val Ser Ser Ser

1080 1085 1090

GCA ACT CAG TAC GGG GCT CAT GAG CAG ACG CAT GCG ATG TAT GCA TGT 3369

Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met Tyr Ala Cys

1095 1100 1105

CCC AAA TTA CCA TAC AAC AAG GAG ACA AGC CCT TCT TTC TAC TTT GCC 3417

Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe Tyr Phe Ala

1110 1115 1120

ATT TCC ACG GGC TCC CTT GCT CAG CAG TAT GCG CAC CCT AAC GCT ACC 3465

Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro Asn Ala Thr

1125 1130 1135

CTG CAC CCA CAT ACT CCA CAC CCT CAG CCT TCA GCT ACC CCC ACT GGA 3513
Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr Pro Thr Gly
1140 1145 1150 1155
CAG CAG CAA AGC CAA CAT GGT GGA AGT CAT CCT GCA CCC AGT CCT GTT 3561
Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro Ser Pro Val
1160 1165 1170
CAG CAC CAT CAG CAC CAG GCC GCC CAG GCT CTC CAT CTG GCC AGT CCA 3609
Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu Ala Ser Pro
1175 1180 1185
CAG CAG CAG TCA GCC ATT TAC CAC GCG GGG CTT GCG CCA ACT CCA CCC 3657
Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro Thr Pro Pro
1190 1195 1200
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1205 1210 1215
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Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro
1220 1225 1230 1235
GCG TAT ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA 3801
Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val
1240 1245 1250
CAG TCA GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG 3849
Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met
1255 1260 1265
CTA ATG ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA 3897
Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln
1270 1275 1280
AGT GCA CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT 3945

Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr

1285 1290 1295

ATG ACG CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG 3987

Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu

1300 1305 1310

TAAGGCTGCC CTGGAGGAAC CGAAAGGCCA AATTCCCTCC TCCCTTCTAC TGCTTCTACC 4047

AACTGGAAGC ACAGAAAACT AGAATTTCAT TTATTTTGTT TTTAAAATAT ATATGTTGAT 4107

TTCTTGTAAC ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGGACCG 4167

AGTAGAGGCA TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC 4227

CGCAGGTACC CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG 4287

AAAGTCATGA ACACATCAGC TAGCAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC 4347

TGCTAAAAAA AAAAAAAAAA 4367

SEQ ID NO: 2

SEQUENCE LENGTH: 203

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

CACCACCAGC AACAGCAACA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG 60

CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG 120

CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG 180

CAGCATCACG GAAACTCTGG GCC 203

SEQ ID NO: 3

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

CACCACCAGC AACAGCAACA 20

SEQ ID NO: 4

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

GGCCCAGAGT TTCCGTGATG 20

SEQ ID NO: 5

SEQUENCE LENGTH: 165

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

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CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG 120

CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAG 165

SEQ ID NO: 6

SEQUENCE LENGTH: 21

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

CCCTCACCAT GTCGCTGAAG C 21

SEQ ID NO: 7

SEQUENCE LENGTH: 19

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

CGACGCTAGA AGGCCGCTG 19

SEQ ID NO: 8

SEQUENCE LENGTH: 19

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

CTTGCGGACA TTGGCAGCC 19

SEQ ID NO: 9

SEQUENCE LENGTH: 27

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

TTCTCTCAGC CAAAGCCTTC TACTACC 27

SEQ ID NO: 10

SEQUENCE LENGTH: 19

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

TATCCGCAGC TCCGCTCCC 19

SEQ ID NO: 11

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRNDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION

AGCCGGGCCG AAACGCGCCG 20

CLAIMS

1. A nucleic acid fragment comprising a nucleic acid region encoding an amino acid sequence shown in SEQ ID NO: 1 (provided that the number of repeat units of Gln from the 166th to 188th amino acid varies between 15 and 100).

2. The nucleic acid fragment according to claim 1, wherein said nucleic acid region is the region from 49nt to 3987nt (provided that the number of repeat units of CAG or CAA in the region from the 543nt to 612nt varies between 15 and 100, and that the CAA in this region may be CAG).

3. A protein having the amino acid sequence encoded by said nucleic acid fragment according to claim 1 or 2.

4. An antibody which undergoes antigen-antibody reaction with said protein according to claim 3.

5. An antisense nucleic acid having a size of not less than 15 bp, which hybridizes with the mRNA transcribed from the nucleic acid fragment according to claim 1 or 2 so as to inhibit translation thereof.

6. A recombinant vector comprising said nucleic acid fragment according to claim 1 or 2 incorporated into an expression vector which can express a desired gene in human body, which recombinant vector can express said nucleic acid fragment in human body.

7. A method comprising introducing said recombinant vector according to claim 6 into human body and

expressing said nucleic acid fragment according to claim 1 or 2 in said human body.

ABSTRACT

A sequence-determined cDNA fragment of the causative gene of SCA2 is disclosed. The cDNA fragment according to the present invention comprises a nucleic acid region encoding an amino acid sequence shown in SEQ ID NO: 1 (provided that the number of repeat units of Gln from the 166th to 188th amino acid varies between 15 and 100).

```
   1 TATCCGCACCTCCGCTCCCACCCGGCGCCTCGGCGCGCCCGCCCTCCGATGCGCTCAGCG
   1          F-1006                                    M  R  S  A
  61 GCCGCAGCTCCTCGGAGTCCCGCGGTGGCCACCGAGTCTCGCCGCTTCGCCGCAGCCAGG
   5 A  A  A  P  R  S  P  A  V  A  T  E  S  R  R  F  A  A  A  R
 121 TGGCCCGGGTGGCGCTCGCTCCAGCGGCCGGCGCGGCGGAGCGGGCGGGGCGGCGGTGGC
  25 W  P  G  W  R  S  L  Q  R  P  A  R  R  S  G  R  G  G  G  G
 181 GCGGCCCCGGGACCGTATCCCTCCGCCGCCCCTCCCCCGCCCGGCCCCGGCCCCCCTCCC
  45 A  A  P  G  P  Y  P  S  A  A  P  P  P  P  G  P  G  P  P  P
 241 TCCCGGCAGAGCTCGCCTCCCTCCGCCTCAGACTGTTTTGGTAGCAACGGCAACGGCGGC
  65 S  R  Q  S  S  P  P  S  A  S  D  C  F  G  S  N  G  N  G  G
 301 GGCGCGTTTCGGCCCGGCTCCCGGCGGCTCCTTGGTCTCGGCGGGCCTCCCCGCCCCTTC
                R-1002
  85 G  A  F  R  P  G  S  R  R  L  L  G  L  G  G  P  P  R  P  F
 361 GTCGTCGTCCTTCTCCCCCTCGCCAGCCCGGGCGCCCCTCCGGCCGCGCCAACCCGCGCC
 105 V  V  V  L  L  P  L  A  S  P  G  A  P  P  A  A  P  T  R  A
 421 TCCCCGCTCGGCGCCCGTGCGTCCCCGCCGCGTTCCGGCGTCTCCTTGGCGCGCCCGGCT
 125 S  P  L  G  A  R  A  S  P  P  R  S  G  V  S  L  A  R  P  A
 481 CCCGGCTGTCCCCGCCCGGCGTGCGAGCCGGTGTATGGGCCCCTCACCATGTCGCTGAAG
                                          F-1
 145 P  G  C  P  R  P  A  C  E  P  V  Y  G  P  L  T  M  S  L  K
 541 CCCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAG
 165 P  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q
 601 CAGCAGCAGCAGCCGCCGCCCGCGGCTGCCAATGTCCGCAAGCCCGGCGGCAGCGGCCTT
                                        R-2
 185 Q  Q  Q  Q  P  P  P  A  A  A  N  V  R  K  P  G  G  S  G  L
 661 CTAGCGTCGCCCGCCGCCGCGCCTTCGCCGTCCTCGTCCTCGGTCTCCTCGTCCTCGGCC
                R-1
 205 L  A  S  P  A  A  A  P  S  P  S  S  S  S  V  S  S  S  S  A
 721 ACGGCTCCCTCCTCGGTGGTCGCGGCGACCTCCGGCGGCGGGAGGCCCGGCCTGGGCAGA
 225 T  A  P  S  S  V  V  A  A  T  S  G  G  G  R  P  G  L  G  R
 781 GGTCGAAACAGTAACAAAGGACTGCCTCAGTCTACGATTTCTTTTGATGGAATCTATGCA
 245 G  R  N  S  N  K  G  L  P  Q  S  T  I  S  F  D  G  I  Y  A
 841 AATATGAGGATGGTTCATATACTTACATCAGTTGTTGGCTCCAAATGTGAAGTACAAGTG
 265 N  M  R  M  V  H  I  L  T  S  V  V  G  S  K  C  E  V  Q  V
 901 AAAAATGGAGGTATATATGAAGGAGTTTTTAAAACTTACAGTCCGAAGTGTGATTTGGTA
 285 K  N  G  G  I  Y  E  G  V  F  K  T  Y  S  P  K  C  D  L  V
 961 CTTGATGCCGCACATGAGAAAAGTACAGAATCCAGTTCGGGGCCGAAACGTGAAGAAATA
 305 L  D  A  A  H  E  K  S  T  E  S  S  S  G  P  K  R  E  E  I
1021 ATGGAGAGTATTTTGTTCAAATGTTCAGACTTTGTTGTGGTACAGTTTAAAGATATGGAC
 325 M  E  S  I  L  F  K  C  S  D  F  V  V  V  Q  F  K  D  M  D
1081 TCCAGTTATGCAAAAAGAGATGCTTTTACTGACTCTGCTATCAGTGCTAAAGTGAATGGC
 345 S  S  Y  A  K  R  D  A  F  T  D  S  A  I  S  A  K  V  N  G
1141 GAACACAAAGAGAAGGACCTGGAGCCCTGGGATGCAGGTGAACTCACAGCCAATGAGGAA
 365 E  H  K  E  K  D  L  E  P  W  D  A  G  E  L  T  A  N  E  E
1201 CTTGAGGCTTTGGAAAATGACGTATCTAATGGATGGGATCCCAATGATATGTTTCGATAT
 385 L  E  A  L  E  N  D  V  S  N  G  W  D  P  N  D  M  F  R  Y
1261 AATGAAGAAAATTATGGTGTAGTGTCTACGTATGATAGCAGTTTATCTTCGTATACAGTG
 405 N  E  E  N  Y  G  V  V  S  T  Y  D  S  S  L  S  S  Y  T  V
```

Fig. 1

```
1321 CCCTTAGAAAGAGATAACTCAGAAGAATTTTTAAAACGGGAAGCAAGGGCAAACCAGTTA
 425 P  L  E  R  D  N  S  E  E  F  L  K  R  E  A  R  A  N  Q  L
1381 GCAGAAGAAATTGAGTCAAGTGCCCAGTACAAAGCTCGAGTGGCCCTGGAAAACGATGAT
 445 A  E  E  I  E  S  S  A  Q  Y  K  A  R  V  A  L  E  N  D  D
1441 AGGAGTGAGGAAGAAAAATACACAGCAGTTCAGAGAAATTCCAGTGAACGTGAGGGGCAC
 465 R  S  E  E  E  K  Y  T  A  V  Q  R  N  S  S  E  R  E  G  H
1501 AGCATAAACACTAGGGAAAATAAATATATTCCTCCTGGACAAAGAAATAGAGAAGTCATA
 485 S  I  N  T  R  E  N  K  Y  I  P  P  G  Q  R  N  R  E  V  I
1561 TCCTGGGGAAGTGGGAGACAGAATTCACCGCGTATGGGCCAGCCTGGATCGGGCTCCATG
 505 S  W  G  S  G  R  Q  N  S  P  R  M  G  Q  P  G  S  G  S  M
1621 CCATCAAGATCCACTTCTCACACTTCAGATTTCAACCCGAATTCTGGTTCAGACCAAAGA
 525 P  S  R  S  T  S  H  T  S  D  F  N  P  N  S  G  S  D  Q  R
1681 GTAGTTAATGGAGGTGTTCCCTGGCCATCGCCTTGCCCATCTCCTTCCTCTCGCCCACCT
 545 V  V  N  G  G  V  P  W  P  S  P  C  P  S  P  S  S  R  P  P
1741 TCTCGCTACCAGTCAGGTCCCAACTCTCTTCCACCTCGGGCAGCCACCCCTACACGGCCG
 565 S  R  Y  Q  S  G  P  N  S  L  P  P  R  A  A  T  P  T  R  P
1801 CCCTCCAGGCCCCCCTCGCGGCCATCCAGACCCCCGTCTCACCCCTCTGCTCATGGTTCT
 585 P  S  R  P  P  S  R  P  S  R  P  P  S  H  P  S  A  H  G  S
1861 CCAGCTCCTGTCTCTACTATGCCTAAACGCATGTCTTCAGAAGGGCCTCCAAGGATGTCC
 605 P  A  P  V  S  T  M  P  K  R  M  S  S  E  G  P  P  R  M  S
1921 CCAAAGGCCCAGCGACATCCTCGAAATCACAGAGTTTCTGCTGGGAGGGGTTCCATATCC
 625 P  K  A  Q  R  H  P  R  N  H  R  V  S  A  G  R  G  S  I  S
1981 AGTGGCCTAGAATTTGTATCCCACAACCCACCCAGTGAAGCAGCTACTCCTCCAGTAGCA
 645 S  G  L  E  F  V  S  H  N  P  P  S  E  A  A  T  P  P  V  A
2041 AGGACCAGTCCCTCGGGGGGAACGTGGTCATCAGTGGTCAGTGGGGTTCCAAGATTATCC
 665 R  T  S  P  S  G  G  T  W  S  S  V  V  S  G  V  P  R  L  S
2101 CCTAAAACTCATAGACCCAGGTCTCCCAGACAGAACAGTATTGGAAATACCCCCAGTGGG
 685 P  K  T  H  R  P  R  S  P  R  Q  N  S  I  G  N  T  P  S  G
2161 CCAGTTCTTGCTTCTCCCCAAGCTGGTATTATTCCAACTGAAGCTGTTGCCATGCCTATT
 705 P  V  L  A  S  P  Q  A  G  I  I  P  T  E  A  V  A  M  P  I
2221 CCAGCTGCATCTCCTACGCCTGCTAGTCCTGCATCGAACAGAGCTGTTACCCCTTCTAGT
 725 P  A  A  S  P  T  P  A  S  P  A  S  N  R  A  V  T  P  S  S
2281 GAGGCTAAAGATTCCAGGCTTCAAGATCAGAGGCAGAACTCTCCTGCAGGGAATAAAGAA
 745 E  A  K  D  S  R  L  Q  D  Q  R  Q  N  S  P  A  G  N  K  E
2341 AATATTAAACCCAATGAAACATCACCTAGCTTCTCAAAAGCTGAAAACAAAGGTATATCA
 765 N  I  K  P  N  E  T  S  P  S  F  S  K  A  E  N  K  G  I  S
2401 CCAGTTGTTTCTGAACATAGAAAACAGATTGATGATTTAAAGAAATTTAAGAATGATTTT
 785 P  V  V  S  E  H  R  K  Q  I  D  D  L  K  K  F  K  N  D  F
2461 AGGTTACAGCCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAG
 805 R  L  Q  P  S  S  T  S  E  S  M  D  Q  L  L  N  K  N  R  E
2521 GGAGAAAAATCAAGAGATTTGATCAAAGACAAAATTGAACCAAGTGCTAAGGATTCTTTC
 825 G  E  K  S  R  D  L  I  K  D  K  I  E  P  S  A  K  D  S  F
2581 ATTGAAAATAGCAGCAGCAACTGTACCAGTGGCAGCAGCAAGCCGAATAGCCCCAGCATT
 845 I  E  N  S  S  S  N  C  T  S  G  S  S  K  P  N  S  P  S  I
```

Fig. 2

```
2641 TCCCCTTCAATACTTAGTAACACGGAGCACAAGAGGGGACCTGAGGTCACTTCCCAAGGG
 865 S  P  S  I  L  S  N  T  E  H  K  R  G  P  E  V  T  S  Q  G
2701 GTTCAGACTTCCAGCCCAGCATGTAAACAAGAGAAAGACGATAAGGAAGAGAAGAAAGAC
 885 V  Q  T  S  S  P  A  C  K  Q  E  K  D  D  K  E  E  K  K  D
2761 GCAGCTGAGCAAGTTAGGAAATCAACATTGAATCCCAATGCAAAGGAGTTCAACCCACGT
 905 A  A  E  Q  V  R  K  S  T  L  N  P  N  A  K  E  F  N  P  R
2821 TCCTTCTCTCAGCCAAAGCCTTCTACTACCCCAACTTCACCTCGGCCTCAAGCACAACCT
F-13 ──────────────────────────►
 925 S  F  S  Q  P  K  P  S  T  T  P  T  S  P  R  P  Q  A  Q  P
2881 AGCCCATCTATGGTGGGTCATCAACAGCCAACTCCAGTTTATACTCAGCCTGTTTGTTTT
 945 S  P  S  M  V  G  H  Q  Q  P  T  P  V  Y  T  Q  P  V  C  F
2941 GCACCAAATATGATGTATCCAGTCCCAGTGAGCCCAGGCGTGCAACCTTTATACCCAATA
 965 A  P  N  M  M  Y  P  V  P  V  S  P  G  V  Q  P  L  Y  P  I
3001 CCTATGACGCCCATGCCAGTGAATCAAGCCAAGACATATAGAGCAGTACCAAATATGCCC
 985 P  M  T  P  M  P  V  N  Q  A  K  T  Y  R  A  V  P  N  M  P
3061 CAACAGCGGCAAGACCAGCATCATCAGAGTGCCATGATGCACCCAGCGTCAGCAGCGGGC
1005 Q  Q  R  Q  D  Q  H  H  Q  S  A  M  M  H  P  A  S  A  A  G
3121 CCACCGATTGCAGCCACCCCACCAGCTTACTCCACGCAATATGTTGCCTACAGTCCTCAG
1025 P  P  I  A  A  T  P  P  A  Y  S  T  Q  Y  V  A  Y  S  P  Q
3181 CAGTTCCCAAATCAGCCCCTTGTTCAGCATGTGCCACATTATCAGTCTCAGCATCCTCAT
1045 Q  F  P  N  Q  P  L  V  Q  H  V  P  H  Y  Q  S  Q  H  P  H
3241 GTCTATAGTCCTGTAATACAGGGTAATGCTAGAATGATGGCACCACCAACACACGCCCAG
1065 V  Y  S  P  V  I  Q  G  N  A  R  M  M  A  P  P  T  H  A  Q
3301 CCTGGTTTAGTATCTTCTTCAGCAACTCAGTACGGGGCTCATGAGCAGACGCATGCGATG
1085 P  G  L  V  S  S  S  A  T  Q  Y  G  A  H  E  Q  T  H  A  M
3361 TATGCATGTCCCAAATTACCATACAACAAGGAGACAAGCCCTTCTTTCTACTTTGCCATT
1105 Y  A  C  P  K  L  P  Y  N  K  E  T  S  P  S  F  Y  F  A  I
3421 TCCACGGGCTCCCTTGCTCAGCAGTATGCGCACCCTAACGCTACCCTGCACCCACATACT
1125 S  T  G  S  L  A  Q  Q  Y  A  H  P  N  A  T  L  H  P  H  T
3481 CCACACCCTCAGCCTTCAGCTACCCCCACTGGACAGCAGCAAAGCCAACATGGTGGAAGT
1145 P  H  P  Q  P  S  A  T  P  T  G  Q  Q  Q  S  Q  H  G  G  S
3541 CATCCTGCACCCAGTCCTGTTCAGCACCATCAGCACCAGGCCGCCCAGGCTCTCCATCTG
1165 H  P  A  P  S  P  V  Q  H  H  Q  H  Q  A  A  Q  A  L  H  L
3601 GCCAGTCCACAGCAGCAGTCAGCCATTTACCACGCGGGGCTTGCGCCAACTCCACCCTCC
1185 A  S  P  Q  Q  Q  S  A  I  Y  H  A  G  L  A  P  T  P  P  S
3661 ATGACACCTGCCTCCAACACGCAGTCGCCACAGAATAGTTTCCCAGCAGCACAACAGACT
1205 M  T  P  A  S  N  T  Q  S  P  Q  N  S  F  P  A  A  Q  Q  T
3721 GTCTTTACGATCCATCCTTCTCACGTTCAGCCGGCGTATACCAACCCACCCCACATGGCC
1225 V  F  T  I  H  P  S  H  V  Q  P  A  Y  T  N  P  P  H  M  A
3781 CACGTACCTCAGGCTCATGTACAGTCAGGAATGGTTCCTTCTCATCCAACTGCCCATGCG
1245 H  V  P  Q  A  H  V  Q  S  G  M  V  P  S  H  P  T  A  H  A
3841 CCAATGATGCTAATGACGACACAGCCACCCGGCGGTCCCCAGGCCGCCCTCGCTCAAAGT
1265 P  M  M  L  M  T  T  Q  P  P  G  G  P  Q  A  A  L  A  Q  S
3901 GCACTACAGCCCATTCCAGTCTCGACAACAGCGCATTTCCCCTATATGACGCACCCTTCA
1285 A  L  Q  P  I  P  V  S  T  T  A  H  F  P  Y  M  T  H  P  S
3961 GTACAAGCCCACCACCAACAGCAGTTGTAAGGCTGCCCTGGAGGAACCGAAAGGCCAAAT
1305 V  Q  A  H  H  Q  Q  Q  L  *
```

Fig. 3

```
4021 TCCCTCCTCCCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAACTAGAATTTCATTTA
4081 TTTTGTTTTTAAAATATATATGTTGATTTCTTGTAACATCCAATAGGAATGCTAACAGTT
4141 CACTTGCAGTGGAAGATACTTGGACCGAGTAGAGGCATTTAGGAACTTGGGGGCTATTCC
4201 ATAATTCCATATGCTGTTTCAGAGTCCCGCAGGTACCCCAGCTCTGCTTGCCGAAACTGG
4261 AAGTTATTTATTTTTTAATAACCCTTGAAAGTCATGAACACATCAGCTAGCAAAAGAAGT
4321 AACAAGAGTGATTCTTGCTGCTATTACTGCT(A)n
```

Fig. 4

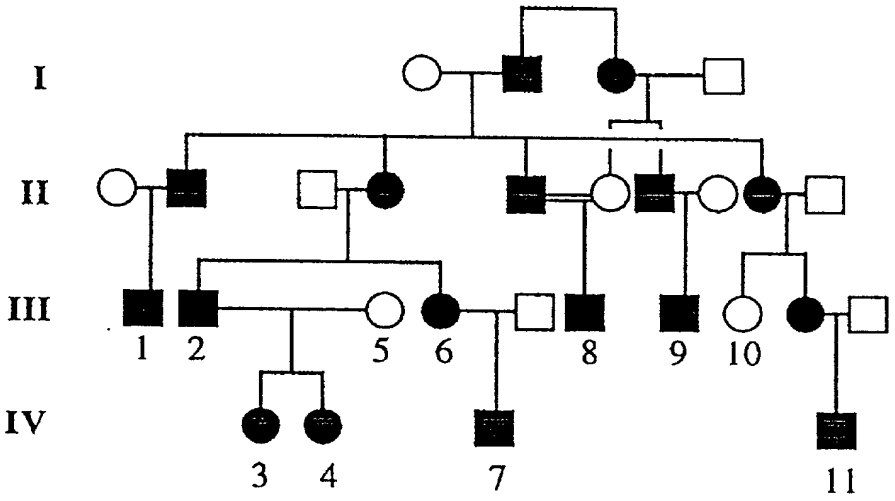

Fig. 5

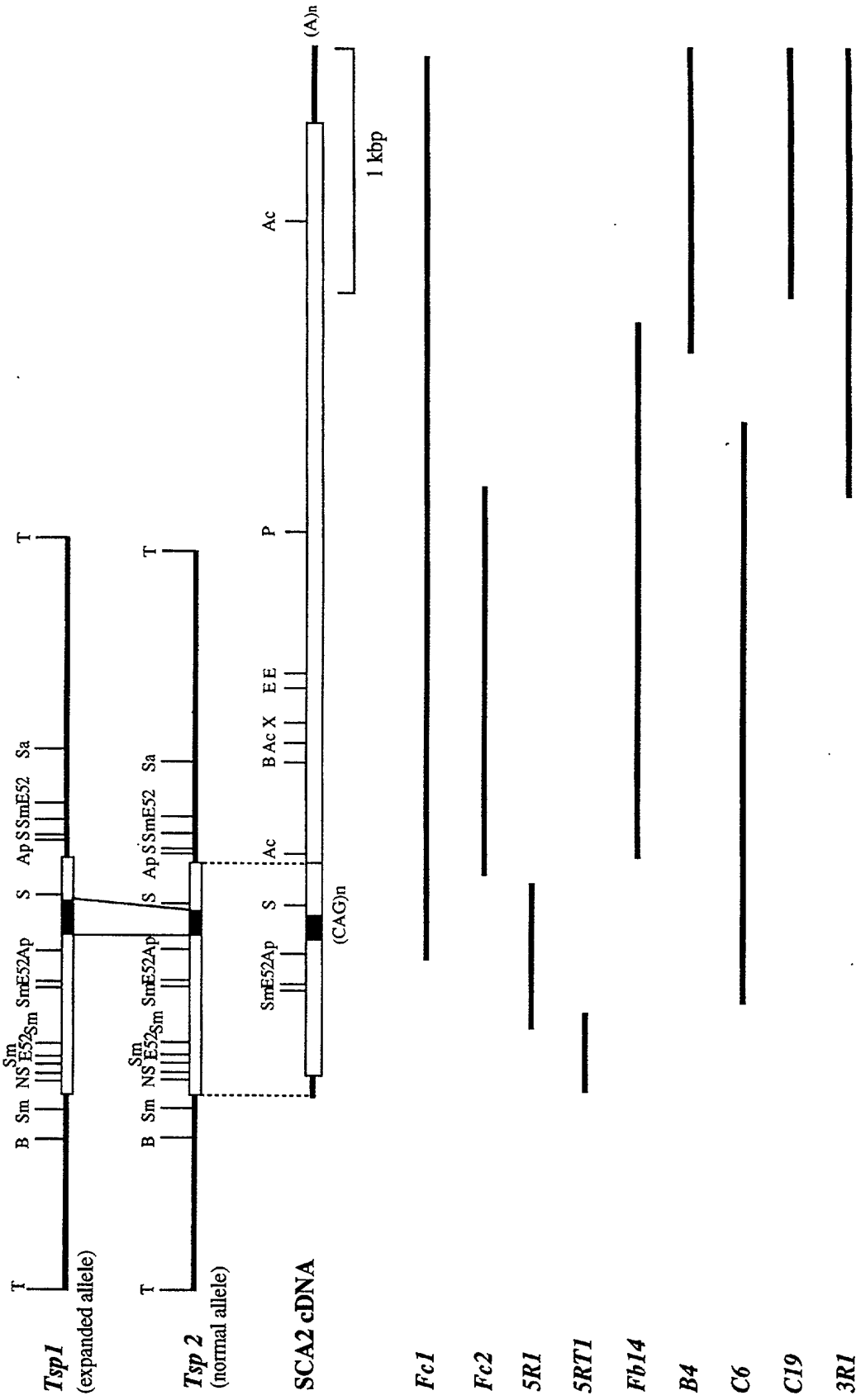
Tsp1
(expanded allele)
Tsp 2
(normal allele)
SCA2 cDNA
(A)n
1 kbp
(CAG)n
T
B
Sm
NS
E52
Sm
SmE52
Ap
S
Sa
Ac
X
E
P
Fc1
Fc2
5R1
5RT1
Fb14
B4
C6
C19
3R1

Fig. 6

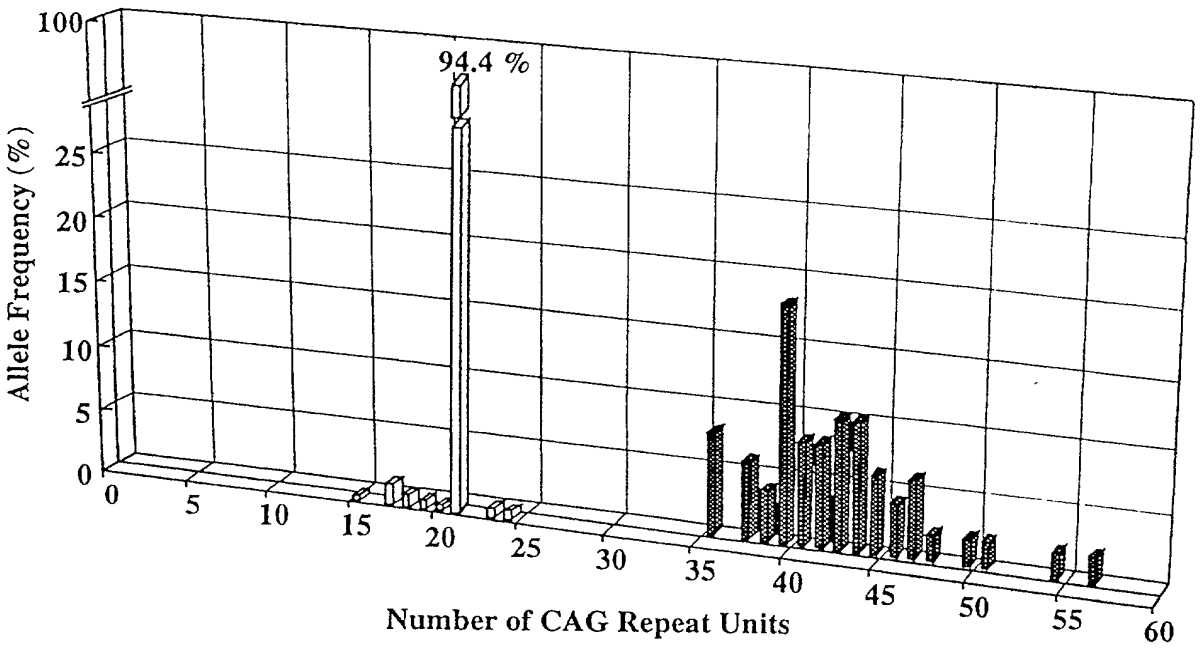

Fig. 7

COMBINED DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that: my residence post office address and citizenship are as stated next to my name;that I verily believe that I am the original, first and sole inventor (if only one inventor is named below) or a joint inventor (if plural inventors are named below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:*"**cDNA Fragment of Causative Gene of Spinocerebellar Ataxia Type 2**"

the specification of which is attached hereto unless one of the following boxes is checked:

☐ The Specification was filed on

and was assigned Serial No. and was amended on

☑ was filed as PCT international application number **PCT/JP97/03946** on **October 30, 1997** and was amended under PCT Article 19 on (if applicable).

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56.

I do not know and do not believe the same was ever known or used in the United States of America before my or our invention thereof, or patented or described in any printed publication in any country before my or our invention thereof, or more than one year prior to this application, that the same was not in public use or on sale in the United States of America more than one year prior to this application, that the invention has not been patented or made the subject of an inventor's certificate issued before the date of this application in any country foreign to the United States of America on an application filed by me or my legal representatives or assigns more than twelve months prior to this application, and that no application for patent or inventor's certificate on this invention has been filed in any country foreign to the United States of America prior to this application by me or my legal representatives or assigns, except as follows:

I hereby claim foreign priority benefits under Title 35, United States Code, § 119 of any foreign application(s) for patent or inventor's certificate listed below:

Prior Foreign Application(s)			Priority Claimed
304059/96	**Japan**	**10.30.96**	**Yes**
(Number)	(Country)	(Month/Day/Year Filed)	

All Foreign Applications, if any, for any Patent or Inventor's Certificate Filed More Than 12 Months Prior To The Filing Date of This Application:

Country	Application No.	Date of Filing (Month/Day/Year)

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, 112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, § 1.56 which occurred between the filing date of the prior application and the national or PCT international filing date of this application:

(Application Serial No.)	(Filing Date)	(Status-patented, pending, abandoned)

I hereby appoint the following attorneys to prosecute this application and/or an international application based on this application and to transact all business in the Patent and Trademark Office connected therewith and in connection with the resulting patent based on instructions received from the entity who first sent the application papers to the attorneys identified below, unless the inventor(s) or assignee provides said attorneys with a written notice to the contrary:

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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